#2   OIPE

RAW SEQUENCE LISTING   DATE: 12/18/2001
PATENT APPLICATION: US/10/008,789 TIME: 16:17:53

Input Set : A:\RTS-0333 Sequence Listing.txt
Output Set: N:\CRF3\12182001\J008789.raw **ENTERED**

```
   6 <110> APPLICANT: C. Frank Bennett
   7         Kenneth Dobie
   9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR
6 EXPRESSION
  11 <130> FILE REFERENCE: RTS-0333
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/008,789
C--> 13 <141> CURRENT FILING DATE: 2001-11-08
  13 <160> NUMBER OF SEQ ID NOS: 89
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 20
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Artificial Sequence
  21 <220> FEATURE:
  23 <223> OTHER INFORMATION: Antisense Oligonucleotide
  25 <400> SEQUENCE: 1
  26 tccgtcatcg ctcctcaggg                                      20
  29 <210> SEQ ID NO: 2
  30 <211> LENGTH: 20
  31 <212> TYPE: DNA
  32 <213> ORGANISM: Artificial Sequence
  34 <220> FEATURE:
  36 <223> OTHER INFORMATION: Antisense Oligonucleotide
  38 <400> SEQUENCE: 2
  39 atgcattctg cccccaagga                                      20
  42 <210> SEQ ID NO: 3
  43 <211> LENGTH: 1755
  44 <212> TYPE: DNA
  45 <213> ORGANISM: Homo sapiens
  47 <220> FEATURE:
  49 <220> FEATURE:
  50 <221> NAME/KEY: CDS
  51 <222> LOCATION: (160)...(1590)
  53 <400> SEQUENCE: 3
  54 cgcccgggca ggtcccaaaa ttaggggga agaggaaaaa aaaaagccag aaaaagtttt    60
  56 cttttctgga gtcccaaacg aggtgcggga cggaagaggg ggtgaaggcc agaggctcgg   120
  58 ggcttcaaga ccgctgtctg agtccccct ttccaggcc atg tcg ggg ccc acc      174
  59                                             Met Ser Gly Pro Thr
  60                                              1               5
  62 tgg ctg ccc ccg aag cag ccg gag ccc gcc aga gcc cct cag ggg agg   222
  63 Trp Leu Pro Pro Lys Gln Pro Glu Pro Ala Arg Ala Pro Gln Gly Arg
  64                10               15                   20
  66 gcg atc ccc cgc ggc acc ccg ggg cca cca ccg gcc cac gga gca gca   270
  67 Ala Ile Pro Arg Gly Thr Pro Gly Pro Pro Pro Ala His Gly Ala Ala
  68             25               30                   35
  70 ctc cag ccc cac ccc agg gtc aat ttt tgc ccc ctt cca tct gag cag   318
  71 Leu Gln Pro His Pro Arg Val Asn Phe Cys Pro Leu Pro Ser Glu Gln
  72          40               45               50
  74 tgt tac cag gcc cca ggg gga ccg gag gat cgg ggg ccg gcg tgg gtg   366
```

```
75 Cys Tyr Gln Ala Pro Gly Gly Pro Glu Asp Arg Gly Pro Ala Trp Val
76       55                    60                 65
78 ggg tcc cat gga gta ctc cag cac acg cag ggg ctc cct gca gac agg      414
79 Gly Ser His Gly Val Leu Gln His Thr Gln Gly Leu Pro Ala Asp Arg
80   70                    75                 80                 85
82 ggg ggc ctt cgc cct gga agc ctg gac gcc gag ata gac ttg ctg agc      462
83 Gly Gly Leu Arg Pro Gly Ser Leu Asp Ala Glu Ile Asp Leu Leu Ser
84                 90                 95                100
86 acc acg ctg gcc aaa ctg aat ggg ggt cgg ggt cat gcg tca cgg cga      510
87 Thr Thr Leu Ala Lys Leu Asn Gly Gly Arg Gly His Ala Ser Arg Arg
88             105                110                115
90 cca gac cga cag gca tat gag ccc ccg cca cct cct gcc tac cgc acg      558
91 Pro Asp Arg Gln Ala Tyr Glu Pro Pro Pro Pro Ala Tyr Arg Thr
92         120                125                130
94 ggc tcc ctg aag cca aat cca gcc tcg ccg ctc cca gcg tct ccc tat      606
95 Gly Ser Leu Lys Pro Asn Pro Ala Ser Pro Leu Pro Ala Ser Pro Tyr
96       135                140                145
98 ggg ggc ccc act cca gcc tct tac act acc gcc agc acc ccg gct ggc      654
99 Gly Gly Pro Thr Pro Ala Ser Tyr Thr Thr Ala Ser Thr Pro Ala Gly
100 150                155                160                165
102 cca gcc ttc ccc gtg caa gtg aag gtg gca cag cca gtg agg ggc tgc     702
103 Pro Ala Phe Pro Val Gln Val Lys Val Ala Gln Pro Val Arg Gly Cys
104                170                175                180
106 ggc cca ccc agg cgg gga gcc tct cag gct tct ggg ccc ctc ccg ggc     750
107 Gly Pro Pro Arg Arg Gly Ala Ser Gln Ala Ser Gly Pro Leu Pro Gly
108             185                190                195
110 ccc cac ttt cct ctc cca ggc cga ggt gaa gtc tgg ggg cct ggc tat     798
111 Pro His Phe Pro Leu Pro Gly Arg Gly Glu Val Trp Gly Pro Gly Tyr
112         200                205                210
114 agg agc cag aga gag cca ggg cca ggg gcc aaa gag gaa gct gct ggg     846
115 Arg Ser Gln Arg Glu Pro Gly Pro Gly Ala Lys Glu Glu Ala Ala Gly
116     215                220                225
118 gtc tct ggc cct gca gga aga gga aga gga ggc gag cac ggg ccc cag     894
119 Val Ser Gly Pro Ala Gly Arg Gly Arg Gly Gly Glu His Gly Pro Gln
120 230                235                240                245
122 gtg ccc ctg agc cag cct cca gag gat gag ctg gat agg ctg acg aag     942
123 Val Pro Leu Ser Gln Pro Pro Glu Asp Glu Leu Asp Arg Leu Thr Lys
124             250                255                260
126 aag ctg gtt cac gac atg aac cac ccg ccc agc ggg gag tac ttt ggc     990
127 Lys Leu Val His Asp Met Asn His Pro Pro Ser Gly Glu Tyr Phe Gly
128             265                270                275
130 cag tgt ggt ggc tgc gga gaa gat gtg gtt ggg gat ggg gct ggg gtt     1038
131 Gln Cys Gly Gly Cys Gly Glu Asp Val Val Gly Asp Gly Ala Gly Val
132       280                285                290
134 gtg gcc ctt gat cgc gtc ttt cac gtg ggc tgc ttt gta tgt tct aca     1086
135 Val Ala Leu Asp Arg Val Phe His Val Gly Cys Phe Val Cys Ser Thr
136       295                300                305
138 tgc cgg gcc cag ctt cgc ggc cag cat ttc tac gcc gtg gag agg agg     1134
139 Cys Arg Ala Gln Leu Arg Gly Gln His Phe Tyr Ala Val Glu Arg Arg
```

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```
140 310                    315                320                325
142 gca tat tgc gag ggc tgc tac gtg gcc acc ctg gag aaa tgt gcc acg    1182
143 Ala Tyr Cys Glu Gly Cys Tyr Val Ala Thr Leu Glu Lys Cys Ala Thr
144                    330                335                340
146 tgc tcc cag ccc atc ctg gac cgg atc ctg cgg gct atg ggg aag gcc    1230
147 Cys Ser Gln Pro Ile Leu Asp Arg Ile Leu Arg Ala Met Gly Lys Ala
148                    345                350                355
150 tac cac cct ggc tgc ttc acc tgc gtg gtg tgt cac cgc ggc ctc gac    1278
151 Tyr His Pro Gly Cys Phe Thr Cys Val Val Cys His Arg Gly Leu Asp
152         360                365                370
154 ggc atc ccc ttc aca gtg gat gct acg agc cag atc cac tgt att gag    1326
155 Gly Ile Pro Phe Thr Val Asp Ala Thr Ser Gln Ile His Cys Ile Glu
156         375                380                385
158 gac ttt cac agg aag ttt gcc cca aga tgc tca gtg tgc ggt ggg gcc    1374
159 Asp Phe His Arg Lys Phe Ala Pro Arg Cys Ser Val Cys Gly Gly Ala
160 390                    395                400                405
162 ata atg cct gag cca ggt cag gag gag act gtg aga att gtt gct ctg    1422
163 Ile Met Pro Glu Pro Gly Gln Glu Glu Thr Val Arg Ile Val Ala Leu
164                    410                415                420
166 gat cga agt ttt cac att ggc tgt tac aag tgc gag gag tgt ggg ctg    1470
167 Asp Arg Ser Phe His Ile Gly Cys Tyr Lys Cys Glu Glu Cys Gly Leu
168         425                430                435
170 ctg ctc tcc tct gag ggc gag tgt cag ggc tgc tac ccg ctg gat ggg    1518
171 Leu Leu Ser Ser Glu Gly Glu Cys Gln Gly Cys Tyr Pro Leu Asp Gly
172         440                445                450
174 cac atc ttg tgc aag gcc tgc agc gcc tgg cgc atc cag gag ctc tca    1566
175 His Ile Leu Cys Lys Ala Cys Ser Ala Trp Arg Ile Gln Glu Leu Ser
176         455                460                465
178 gcc acc gtc acc act gac tgc tga gtcttcctag aagtacctgc tgggttctca   1620
179 Ala Thr Val Thr Thr Asp Cys
180 470                    475
182 gttccagttc ccatcctttg attgatcact ctccctgaca tccacctgta tgactttgtc   1680
184 accaaatgct gtcttctctt tctccaatca agaaataata atccctcgag tttacaaaaa   1740
186 aaaaaaaaaa aaaaa                                                    1755
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 20
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR Primer
198 <400> SEQUENCE: 4
199 gctgcggaga agatgtggtt                                                20
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 21
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
209 <223> OTHER INFORMATION: PCR Primer
211 <400> SEQUENCE: 5
```

```
       212 gcccggcatg tagaacatac a                              21
       215 <210> SEQ ID NO: 6
       216 <211> LENGTH: 23
       217 <212> TYPE: DNA
       218 <213> ORGANISM: Artificial Sequence
       220 <220> FEATURE:
       222 <223> OTHER INFORMATION: PCR Probe
       224 <400> SEQUENCE: 6
       225 ttgatcgcgt ctttcacgtg ggc                            23
       228 <210> SEQ ID NO: 7
       229 <211> LENGTH: 19
       230 <212> TYPE: DNA
       231 <213> ORGANISM: Artificial Sequence
       233 <220> FEATURE:
       235 <223> OTHER INFORMATION: PCR Primer
       237 <400> SEQUENCE: 7
       238 gaaggtgaag gtcggagtc                                 19
       241 <210> SEQ ID NO: 8
       242 <211> LENGTH: 20
       243 <212> TYPE: DNA
       244 <213> ORGANISM: Artificial Sequence
       246 <220> FEATURE:
       248 <223> OTHER INFORMATION: PCR Primer
       250 <400> SEQUENCE: 8
       251 gaagatggtg atgggatttc                                20
       254 <210> SEQ ID NO: 9
       255 <211> LENGTH: 20
       256 <212> TYPE: DNA
       257 <213> ORGANISM: Artificial Sequence
       259 <220> FEATURE:
       261 <223> OTHER INFORMATION: PCR Probe
       263 <400> SEQUENCE: 9
       264 caagcttccc gttctcagcc                                20
       267 <210> SEQ ID NO: 10
       268 <211> LENGTH: 7001
       269 <212> TYPE: DNA
       270 <213> ORGANISM: Homo sapiens
       272 <220> FEATURE:
       274 <221> NAME/KEY: exon
       275 <222> LOCATION: (486)...(740)
       276 <223> OTHER INFORMATION: exon 1
W--> 278 <221> NAME/KEY: exon:intron junction
       279 <222> LOCATION: (740)...(741)
       280 <223> OTHER INFORMATION: exon 1:intron 1
       282 <221> NAME/KEY: intron
       283 <222> LOCATION: (741)...(994)
       284 <223> OTHER INFORMATION: intron 1
W--> 286 <221> NAME/KEY: intron:exon junction
       287 <222> LOCATION: (994)...(995)
```

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```
         288 <223> OTHER INFORMATION: intron 1:exon 2
         290 <221> NAME/KEY: exon
         291 <222> LOCATION: (995)...(1122)
         292 <223> OTHER INFORMATION: exon 2
W--> 294 <221> NAME/KEY: exon:intron junction
         295 <222> LOCATION: (1122)...(1123)
         296 <223> OTHER INFORMATION: exon 2:intron 2
         298 <221> NAME/KEY: intron
         299 <222> LOCATION: (1123)...(1241)
         300 <223> OTHER INFORMATION: intron 2
W--> 302 <221> NAME/KEY: intron:exon junction
         303 <222> LOCATION: (1241)...(1242)
         304 <223> OTHER INFORMATION: intron 2:exon 3
         306 <221> NAME/KEY: exon
         307 <222> LOCATION: (1242)...(1367)
         308 <223> OTHER INFORMATION: exon 3
W--> 310 <221> NAME/KEY: exon:intron junction
         311 <222> LOCATION: (1367)...(1368)
         312 <223> OTHER INFORMATION: exon 3:intron 3
         314 <221> NAME/KEY: intron
         315 <222> LOCATION: (1368)...(1628)
         316 <223> OTHER INFORMATION: intron 3
W--> 318 <221> NAME/KEY: intron:exon junction
         319 <222> LOCATION: (1628)...(1629)
         320 <223> OTHER INFORMATION: intron 3:exon 4
         322 <221> NAME/KEY: exon
         323 <222> LOCATION: (1629)...(2000)
         324 <223> OTHER INFORMATION: exon 4
W--> 326 <221> NAME/KEY: exon:intron junction
         327 <222> LOCATION: (2000)...(2001)
         328 <223> OTHER INFORMATION: exon 4:intron 4
         330 <221> NAME/KEY: intron
         331 <222> LOCATION: (2001)...(3503)
         332 <223> OTHER INFORMATION: intron 4
W--> 334 <221> NAME/KEY: intron:exon junction
         335 <222> LOCATION: (3503)...(3504)
         336 <223> OTHER INFORMATION: intron 4:exon 5
         338 <221> NAME/KEY: exon
         339 <222> LOCATION: (3504)...(3597)
         340 <223> OTHER INFORMATION: exon 5
W--> 342 <221> NAME/KEY: exon:intron junction
         343 <222> LOCATION: (3597)...(3598)
         344 <223> OTHER INFORMATION: exon 5:intron 5
         346 <221> NAME/KEY: intron
         347 <222> LOCATION: (3598)...(3707)
         348 <223> OTHER INFORMATION: intron 5
W--> 350 <221> NAME/KEY: intron:exon junction
         351 <222> LOCATION: (3707)...(3708)
         352 <223> OTHER INFORMATION: intron 5:exon 6
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VERIFICATION SUMMARY   DATE: 12/18/2001
PATENT APPLICATION: US/10/008,789   TIME: 16:17:54

Input Set : A:\RTS-0333 Sequence Listing.txt
Output Set: N:\CRF3\12182001\J008789.raw

```
L:13  M:270 C: Current Application Number differs, Replaced Current Application No
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:286 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:294 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:302 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:310 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:318 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:334 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:342 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:350 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:366 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:374 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:382 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:398 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
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